

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/510,411
Source: pt/10
Date Processed by STIC: 4/21/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/510,411

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 04/21/2005

PATENT APPLICATION: US/10/510,411

TIME: 09:57:42

Input Set : A:\Type-I Diabetes.ST25.txt

Output Set: N:\CRF4\04212005\J510411.raw

3 <110> APPLICANT: The Curators of the University of Missouri
 5 <120> TITLE OF INVENTION: Treatment of Type I Diabetes Before and After Expression of
 6 Predisposition Markers
 8 <130> FILE REFERENCE: 04343407
 10 <140> CURRENT APPLICATION NUMBER: 10/510,411
 11 <141> CURRENT FILING DATE: 2004-10-06
 13 <150> PRIOR APPLICATION NUMBER: 60/371,663
 14 <151> PRIOR FILING DATE: 2002-04-09
 16 <150> PRIOR APPLICATION NUMBER: PCT/US2003/010700
 17 <151> PRIOR FILING DATE: 2002-04-08
 19 <160> NUMBER OF SEQ ID NOS: 5
 21 <170> SOFTWARE: PatentIn version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 15
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Gallus sp.
 29 <220> FEATURE:
 30 <221> NAME/KEY: MISC_FEATURE
 31 <222> LOCATION: (9)..(23) *only 15 amino acids in this sequence*
 32 <223> OTHER INFORMATION: Insulin is conserved among species
 34 <400> SEQUENCE: 1
 36 Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Gln Arg Gly
 37 1 5 10 15
 40 <210> SEQ ID NO: 2
 41 <211> LENGTH: 15
 42 <212> TYPE: PRT
 43 <213> ORGANISM: various species *invalid <2137 response*
 46 <220> FEATURE:
 47 <221> NAME/KEY: MISC_FEATURE
 48 <222> LOCATION: (11)..(25) *see item 10 on Error Summary Sheet*
 49 <223> OTHER INFORMATION: Amino acid residues 11-25 of HEL.
 51 <400> SEQUENCE: 2
 53 Ala Met Lys Arg His Gly Leu Asp Asn Tyr Arg Gly Arg Ser Leu
 54 1 5 10 15
 57 <210> SEQ ID NO: 3
 58 <211> LENGTH: 20
 59 <212> TYPE: PRT
 60 <213> ORGANISM: various species
 63 <220> FEATURE:
 64 <221> NAME/KEY: MISC_FEATURE
 65 <222> LOCATION: (524)..(543)
 66 <223> OTHER INFORMATION: Amino acid residues 524 -543 of GAD 65
 68 <400> SEQUENCE: 3

pp 1-2
 Does Not Comply
 Detected Diskette Needs

*do you mean
 (1)..(15)?
 or (9)..(23)
 of another,
 larger sequence?*

*if this
 sequence was
 synthesized from
 various species,
 use <2137> Artificial Sequence
 and <2207> (header only)
 <2237> synthesized
 from various species 4/21/05*

RAW SEQUENCE LISTING

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Input Set : A:\Type-I Diabetes.ST25.txt

Output Set: N:\CRF4\04212005\J510411.raw

70 Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Gln
71 1 5 10 15
74 Tyr Gly Thr Thr
75 20
78 <210> SEQ ID NO: 4
79 <211> LENGTH: 15
80 <212> TYPE: PRT
81 <213> ORGANISM: various species
84 <220> FEATURE:
85 <221> NAME/KEY: MISC FEATURE
86 <222> LOCATION: (206)..(220)
87 <223> OTHER INFORMATION: Amino Acid Residues 206-220 of GAD 65
89 <400> SEQUENCE: 4
91 Thr Tyr Glu Ile Ala Pro Val Phe Val Leu Leu Glu Tyr Val Thr
92 1 5 10 15
95 <210> SEQ ID NO: 5
96 <211> LENGTH: 18
97 <212> TYPE: PRT
98 <213> ORGANISM: various species
101 <220> FEATURE:
102 <221> NAME/KEY: MISC FEATURE
103 <223> OTHER INFORMATION: Flanking regions
105 <400> SEQUENCE: 5
107 Tyr Phe Cys Ala Arg Ser Tyr Tyr Ser Gly Asp Met Tyr Cys Phe Asp
108 1 5 10 15
111 Tyr Trp

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/510,411

DATE: 04/21/2005

TIME: 09:57:43

Input Set : A:\Type-I Diabetes.ST25.txt

Output Set: N:\CRF4\04212005\J510411.raw